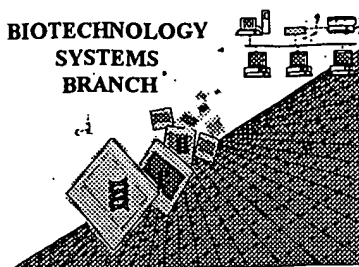


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/909,574
Source: OLP
Date Processed by STIC: 8/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 08/01/2001

PATENT APPLICATION: US/09/909,574

TIME: 15:04:48

Input Set : A:\909574.txt

Output Set: N:\CRF3\08012001\I909574.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Skraly, Frank A.
 4 Sholl, Martha
 6 <120> TITLE OF INVENTION: Production of Polyhydroxyalkanoates From Polyols
 8 <130> FILE REFERENCE: MBX 039
 10 <140> CURRENT APPLICATION NUMBER: US/09/909,574
 12 <141> CURRENT FILING DATE: 2001-07-20
 14 <150> PRIOR APPLICATION NUMBER: 60/219,995
 16 <151> PRIOR FILING DATE: 2000-07-21
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: Microsoft Word

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
 24 <211> LENGTH: 44
 26 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 34 <400> SEQUENCE: 1
 E--> 36 5'-tctctgaattcaaggaggaa⁴aaat⁴atgaag⁴tatt⁴aaat⁴ggc-3'
 delete 38 <210> SEQ ID NO: 2
 40 <211> LENGTH: 34
 42 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence
 46 <220> FEATURE:
 48 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 50 <400> SEQUENCE: 2
 E--> 52 5'-tttctctgagctcg⁴gatatt⁴ta⁴atgatt⁴gtagg-3'
 54 <210> SEQ ID NO: 3
 56 <211> LENGTH: 47
 58 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 64 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 66 <400> SEQUENCE: 3
 E--> 68 5'-ggtggtac⁴cttaagaggaggt⁴ttttatgaatt⁴ttcatcacctggc⁴tt-3'
 70 <210> SEQ ID NO: 4
 72 <211> LENGTH: 32
 74 <212> TYPE: DNA
 76 <213> ORGANISM: Artificial Sequence
 78 <220> FEATURE:
 80 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 82 <400> SEQUENCE: 4:
 E--> 84 5'-ggtgcggccgctcaggcctccaggc⁴ttatcca-3'
 86 <210> SEQ ID NO: 5

Please consult sequence
Rules for valid
format.

Per 1.822 of sequence Rules, group
all non-coding bases into groups of 10,
with a space between
groups.

44 ← insert cumulative
 base
 do not show primer marker total
at
right
margin
of each
line

same error

same

same

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/909,574

DATE: 08/01/2001

TIME: 15:04:48

Input Set : A:\909574.txt

Output Set: N:\CRF3\08012001\I909574.raw

88 <211> LENGTH: 57
 90 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 96 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 98 <400> SEQUENCE: 5
 E--> 100 5'-cctgaattcaggagggtttttatggcggtttatctactatctgacccac-3' *same*
 102 <210> SEQ ID NO: 6
 104 <211> LENGTH: 32
 106 <212> TYPE: DNA
 108 <213> ORGANISM: Artificial Sequence
 110 <220> FEATURE:
 112 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 114 <400> SEQUENCE: 6
 E--> 116 5'-cctgagctcctacctgcaagtgtctgcgcgctc-3' *same*
 118 <210> SEQ ID NO: 7
 120 <211> LENGTH: 49
 122 <212> TYPE: DNA
 124 <213> ORGANISM: Artificial Sequence
 126 <220> FEATURE: *same*
 128 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 130 <400> SEQUENCE: 7
 E--> 132 5'-tcccctaggattcaggagggtttttatgggagtgggaagagatatataaag-3'
 134 <210> SEQ ID NO: 8
 136 <211> LENGTH: 38
 138 <212> TYPE: DNA
 140 <213> ORGANISM: Artificial Sequence
 142 <220> FEATURE: *same*
 144 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA primer
 146 <400> SEQUENCE: 8
 E--> 148 5'-ccttaagtcgacaaattctaaaatctatttttaattc-3'
 E--> 155 ATL1 #473506 v1
 E--> 156 1

*delete**PMI*

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/909,574

DATE: 08/01/2001

TIME: 15:04:49

Input Set : A:\909574.txt

Output Set: N:\CRF3\08012001\I909574.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:1
L:36 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:36 M:112 C: (48) String data converted to lower case,
L:36 M:252 E: No. of Seq. differs, <211>LENGTH:Input:44 Found:48 SEQ:1
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:38 SEQ:2
L:52 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=2
L:52 M:252 E: No. of Seq. differs, <211>LENGTH:Input:34 Found:38 SEQ:2
L:68 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:51 SEQ:3
L:68 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=3
L:68 M:252 E: No. of Seq. differs, <211>LENGTH:Input:47 Found:51 SEQ:3
L:84 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:4
L:84 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=4
L:84 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:36 SEQ:4
L:100 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:51 SEQ:5
L:100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=5
L:100 M:252 E: No. of Seq. differs, <211>LENGTH:Input:57 Found:51 SEQ:5
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:6
L:116 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=6
L:116 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:36 SEQ:6
L:132 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:53 SEQ:7
L:132 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=7
L:132 M:252 E: No. of Seq. differs, <211>LENGTH:Input:49 Found:53 SEQ:7
L:148 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:8
L:148 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=8
M:254 Repeated in SeqNo=8
L:155 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:156 M:252 E: No. of Seq. differs, <211>LENGTH:Input:38 Found:47 SEQ:8